



FIGURE 1 (1/2)

|                              |   |     |
|------------------------------|---|-----|
| (SEQ ID NO: 9) {CAA69226}    | 1   | 50  |
| (SEQ ID NO: 2) {PRSS11-Like} | MQIPRAALLP LLLLLLAAPA SAQLSRAGRS APLAAGCPDR CEPARCPPQP  |     |
| (SEQ ID NO: 10) {AAB94569}   | -----   |     |
| Consensus                    | -----MAAPRAGRG AGWSLRAWRA LGGIRWGRRP                    |     |
|                              | -----   |     |
|                              | 51  | 100 |
| {CAA69226}                   | EHCEGGRARD ACGCCEVCGA PEGAACGLQE GPCGEGLCV VPFGVPASAT   |     |
| {PRSS11-Like}                | -----   |     |
| {AAB94569}                   | RLTPDLRALL TSGTSD...P RARVTYGTGS LWARLSVGVT EPRACLTSGT  |     |
| Consensus                    | -----   |     |
|                              | 101   | 150 |
| {CAA69226}                   | VRRRAQAGLC VCASSEPVCG SDANTYANLC QLRAASRRSE RLHRPPVIVL  |     |
| {PRSS11-Like}                | -----   |     |
| {AAB94569}                   | PGPRAQLTAV TPDTRTREAS ENSGTRSRAW LAVALGAGGA VLLLLWGGR   |     |
| Consensus                    | -----   |     |
|                              | 151   | 200 |
| {CAA69226}                   | ORGACGQQQE D..PNSLRHK YNFIADVVEK IAPAVVHIEL FRKLPPFSKRE |     |
| {PRSS11-Like}                | ALPA.SAGLH Q..LSSPRYK FNFIADVVEK IAPAVVHIEL FLRHPLFGRN  |     |
| {AAB94569}                   | GPPAVLAAVP SPPPASPRSQ YNFIADVVEK TAPAVVYIEI LDRHPFLGRE  |     |
| Consensus                    | ---A-----S-R-- -NFIADVVEK -APAVV-IE- ----P---R-         |     |
|                              | 201   | 250 |
|                              | *   |     |
| {CAA69226}                   | VPVASGSGFI VSEDGLIVTN AHVVTN.... ..KHRVKVEL KNGATYEAKI  |     |
| {PRSS11-Like}                | VPLSSGSGFI MSEAGLIITN AHVVSSNSAA PGRQQLKVQL QNGDSYEATI  |     |
| {AAB94569}                   | VPISNGSGFV VAADGLIVTN AHVVAD.... ..RRRVVRVL LSGDTYEAVV  |     |
| Consensus                    | VP---GSGF- ----GLI-TN AHVV-----V-L --G--YEA--           |     |

FIGURE 1 (2/2)

|               |             |                        |                        |
|---------------|-------------|------------------------|------------------------|
|               | 251         | *                      | 300                    |
| {CAA69226}    | KDVDEKADIA  | LIKIDHQGKL PVLLLGSRSE  | LRPGEFVVAI GSPFSLQNTV  |
| {PRSS11-Like} | KDIDKKS DIA | TIKIHPPKKL PVLLLGHSAD  | LRPGEFVVAI GSPFALQNTV  |
| {AAB94569}    | TAVDPVADIA  | TLRIQTKEPL PTLPLGRSAD  | VRQGEFVVAM GSPFALQNTI  |
| Consensus     | ---D---DIA  | ---I-----L P-L-LG-S--- | -R-GEFVVA- GSPF-LQNT-  |
|               | 301         | *                      | 350                    |
| {CAA69226}    | TTGIVSTTQR  | GGKELGLRNS DMDYIQTDAI  | INYGNSSGGPL VNLDGEVIGI |
| {PRSS11-Like} | TTGIVSTAQR  | EGRELGLRDS DMDYIQTDAI  | INYGNSSGGPL VNLDGEVIGI |
| {AAB94569}    | TSGIVSSAQR  | PARDLGLPQT NVEYIQTDAI  | IDFGNSSGGPL VNLDGEVIGV |
| Consensus     | T-GIVS--QR  | ----LGL--- ---YIQTDA-  | I--GNSGGPL VNLDGEVIG-  |
|               | 351         |                        | 400                    |
| {CAA69226}    | NTLKVTAGIS  | FAIPSDKIKK FLTESHDR.Q  | AKGKAITKKK YIGIRMSLT   |
| {PRSS11-Like} | NTLKVTAGIS  | FAIPSDRITR FLTEFQDK.Q  | IKD...WKKR FIGIRMRTIT  |
| {AAB94569}    | NTMKVTAGIS  | FAIPSDRLRE FLHRGEKKNS  | SSGISGSQRR YIGVMMLTSL  |
| Consensus     | NT-KVTAGIS  | FAIPSD---- FL-----     | ----- -IG--M----       |
|               | 401         |                        | 450                    |
| {CAA69226}    | SSKAKELKDR  | HRDFPDVISG AYIIEVIPDT  | PAEAGGLKEN DVIISINGQS  |
| {PRSS11-Like} | PSLVDELKAS  | NPDFPEVSSG IYVQEVAPNS  | PSQGGIQDG DIIVKVNGRP   |
| {AAB94569}    | PSILAEQLR   | EPSFPDVQHG VLIHKVILGS  | PAHRAGLRPG DVILAIGEQM  |
| Consensus     | -S---EL---  | ---FP-V--G -----V----  | P----G---- D-I-----    |
|               | 451         |                        | 489                    |
| {CAA69226}    | VVSANDVSDV  | IKRESTLMV VRRGNEDIMI   | TVIPERIDP              |
| {PRSS11-Like} | LVDSSSELQEA | VLTESPLLE VRRGNDDLLE   | SIAPEVVM-              |
| {AAB94569}    | VQNAEDVYEA  | VRTQSQLAVQ IRRGRETLTL  | YVTPEVTE-              |
| Consensus     | -----       | ----S-L--- -RRG-----   | ---PE----              |

FIGURE 2 (1/1)

HtrA3 (BC034390) (SEQ ID NO: 11) x PRSS11-Like (SEQ ID NO: 2)

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101 CALQAASRRALQLSGTPVRQLQKGACP..LGLHQLSSPRYKFNFIADVVE 148
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  .....MHLALPASAGLHQLSSPRYKFNFIADVVE 29

149 KIAPAVVHIELFLRHPLFGRNVPLSSSGSFIMSEAGLIITNAHVSSNSA 198
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
30 KIAPAVVHIELFLRHPLFGRNVPLSSSGSFIMSEAGLIITNAHVSSNSA 79

199 APGRQQLKVQLONGDSYEATIKDIDKKSDIATIKIHPKKKLPVLLLGHSA 248
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
80 APGRQQLKVQLONGDSYEATIKDIDKKSDIATIKIHPKKKLPVLLLGHSA 129

249 DLRPGFEFVVAIGSPFALQNTVTTGIVSTAQREGRELGLRDSMDYIQTDA 298
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
130 DLRPGFEFVVAIGSPFALQNTVTTGIVSTAQREGRELGLRDSMDYIQTDA 179

299 IINYGNSSGGPLVNLGDEVIGINTLKVTTAGISFAIPSDRITRFLTEFQDKQ 348
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
180 IINYGNSSGGPLVNLGDEVIGINTLKVTTAGISFAIPSDRITRFLTEFQDKQ 229

349 IKDWKKRFIGIRMRTITPSLVDELKASNPDFPEVSSGIYVQEVAPNSPSQ 398
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
230 IKDWKKRFIGIRMRTITPSLVDELKASNPDFPEVSSGIYVQEVAPNSPSQ 279

399 RGGIQDGDIIIVKNGRPLVDSSSELQEAVLTESPLLEVRNGNDDLFSIA 448
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
280 RGGIQDGDIIIVKNGRPLVDSSSELQEAVLTESPLLEVRNGNDDLFSIA 329

449 PEVVM 453
      | | | |
330 PEVVM 334
```

FIGURE 4

**A. Unique HtrA3 Long Form Exons**

|                 |  |           |    |                 |
|-----------------|--|-----------|----|-----------------|
|                 | E1 589-bp  | 12,083-bp | E2 |                 |
| (SEQ ID NO: 12) | GCGCCTGCCCCGTTGGgtaagcgctcggggg... ..ttcccgccagcgagGTCTCCACCAGCTGA |           |    | (SEQ ID NO: 13) |
|                 | E2 100-bp  | 4,024-bp  | E3 |                 |
| (SEQ ID NO: 14) | AGAGCTCTTCTGAGgtgggtgaatacccc... ..tctccctggctgcagACACCCGCTGTTTGG  |           |    | (SEQ ID NO: 15) |

**B. Unique PRSS11-Like Exon**

|                 |   |          |    |                 |
|-----------------|---|----------|----|-----------------|
|                 | E1 1,138-bp   | 4,024-bp | E2 |                 |
| (SEQ ID NO: 16) | AGAGCTCTTCTGAGgtgggtgaatacccc... ..tctccctggctgcagACACCCGCTGTTTGG |          |    | (SEQ ID NO: 17) |

**C. Common HtrA3 Long form and PRSS11-Like Exons**

|                 |  |           |               |                 |
|-----------------|--|-----------|---------------|-----------------|
| (SEQ ID NO: 18) | E3/E2 223-bp   | 4,586-bp  | E4/E3         | (SEQ ID NO: 19) |
|                 | AAGATCCATCCCAAGgtgggtgggcgtggg... ..ccttctctctcctagAAAAAGCTCCCTGTG |           |               |                 |
| SEQ ID NO: 20)  | E4/E3 195-bp   | 756-bp    | E5/E4         | (SEQ ID NO: 21) |
|                 | GATGCCATCATCAACgtgagtgcccaggac... ..ttcctccccttgagTACGGGAAGTCCGGG  |           |               |                 |
| (SEQ ID NO: 22) | E5/E4 33-bp  | 1,733-bp  | E6/E5         | (SEQ ID NO: 23) |
|                 | CCACTGGTGAACCTGgtaagtgtcccctag... ..tacctccctgcccagGATGGCGAGGTCATT |           |               |                 |
| (SEQ ID NO: 24) | E6/E5 115-bp   | 90,643-bp | E7/E6         | (SEQ ID NO: 25) |
|                 | ACAAGCAGATCAAAGgtaaagagctcacct... ..gtgtttcatttccagACTGGAAGAAGCGCT |           |               |                 |
| (SEQ ID NO: 26) | E7/E6 49-bp  | 1,672-bp  | E8/E7         | (SEQ ID NO: 27) |
|                 | GACGATCACACCAAGgtgagtgctgaaga... ..gcagactctttccagCCTGGTGGATGAGCT  |           |               |                 |
| (SEQ ID NO: 28) | E8/E7 96-bp  | 1,691-bp  | E9/E8 1140-bp | (SEQ ID NO: 29) |
|                 | TTCACCTTCTCAGAGgtaggctctgccaga... ..ctctcctgttggcagAGGCGGCATCCAAGA |           |               |                 |

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